

# human neutral Sphingomyelinase (NSM) Gene Sequence

1	ACCGCGGCCGTCGCTGGAGAGTTCGAGCCCCCTAGCGCCCCTGGAGCTCCCCAACCATGA	60
	TGGCGCCGGCAGCGACCTCTCAAGCTCGGCGGATCGCGGGGACCTCGAGGGGTTGGTACT	ΕI
61	AGCCCAACTTCTCCCTGCGACTGCGGATCTTCAACCTCAACTGCTGGTGAGTGCGTCTGC	120
	TCGGGTTGAAGAGGGACGCTGACGCCTAGAAGTTGGAGTTGACGACCACTCACGCAGACG	
121	GGAGTGCGGTCTGGGGGCCACCTTCCGTTCGCACCCATGCAGCCTTCCTCCCCCTATCCC	180
	CCTCACGCCAGACCCCCGGTGGAAGGCAAGCGTGGGTACGTCGGAAGGAGGGGGATAGGG	
181	GCCCCACGATCTCAGGGTGTAGGGAAAACCCGAACCTCCAAAGTCCACATCTGGCCCCAG	240
	CGGGGTGCTAGAGTCCCACATCCCTTTTGGGCTTGGAGGTTTCAGGTGTAGACCGGGGTC	
241	CGCCGGTGGTCCCAGCAGTCGCCTCCCCTGCCCCGCTCTTCCCTTAGGGGCATTCC	300
	GCGGCCACCAGGGTCGTCAGCGGAGGGGACGGGGCGAGAAGGGAATCCCCGTAAGG	
301	GTACTTGAGCAAGCACCGGGCCGACCGCATGAGGCGCCTGGGAGACTTTCTGAACCAGGA	360
	CATGAACTCGTTCGTGGCCCGGCTGCCTACTCCGCGGACCCTCTGAAAGACTTGGTCCT	ЕП
361	GAGCTTCGACCTGGCTTTGCTGGAGGAGGTGAGATTGTGCAGCACGGTGCGGAACCCAGG	420
	$\tt CTCGAAGCTGGACCGAAACGACCTCCTCCACTCTAACACGTCGTGCCACGCCTTGGGTCC$	
421	CTGGGAGGAGGACAGCCGTCCCACTGGGGAAAGACCAAGCAGGCATCCTCACCGCTTC	480
	${\tt GACCCTCCTCTCTGGCAGGGTGACCCCTTTCTGGTTCGTCCGTAGGAGTGGCGAAG}$	
481	CCTCAGGTGTGGAGTGAGCAGGACTTCCAGTACCTGAGACAGAAGCTGTCACCTACCT	540
	GGAGTCCACACCTCACTCGTCCTGAAGGTCATGGACTCTGTCTTCGACAGTGGATGGA	ЕШ
541	CCAGCTGCACACCACTTCCGGAGGTGAGAAGCCCACTGGCCTGAAGCCTGTTGTCATCCC	600
541	GCTCGACGTGTGGTGAAGGCCTCCACTCTTCGGGTGACCGGACTTCGGACAACAGTAGGG	600
601	AGGAGGCTCTTGGCCCTGCCAGCCCTTCCCTATCCTGCACTCTCCAGTCTCCTCCA	660
	${\tt TCCTCCGAGAACCGGGACGGTCGGGAAGGGATAGGACGGAC$	
661	GCCTCCTCTCCCTCTGGATGTGAGAGAAGGAGAAGGGTGAACCAAGAAGGTCCTATGACT	720
	$\tt CGGAGGAGAGGGAGACCTACACTCTCTTCCTCTTCCCACTTGGTTCTTCCAGGATACTGA$	
721	TCAGCCCATTTCAGCTTTGTTTTCTGGCTGCCCTATACTCCTCCAAAGGCCGTCGCCTTG	780
	AGTCGGGTAAAGTCGAAACAAAAGACCGACGGGATATGAGGAGGTTTCCGGCAGCGGAAC	
781	GTTCTAGGGCTAGTCCCAGCAGTAGAAAAAGAAAAAAATAGCTGATCAGAGCTGGAAGAC	840
	CAAGATCCCGATCAGGGTCGTCATCTTTTTTTTTTTTTT	
841	AAGGGAGGGAAGAAGGCTGGGTGTCTCTCCCTGTTTTTCTGGTTATTAAGCAGGGCTTG	900
	TTCCCTCCCCTTCTTCCGACCCACAGAGAGGGGACAAAAAAGACCAATAATTCGTCCCGAAC	

Figure 1-1

2 / 12 CTCTCCCTCCTTCTCCCCCACATCCTAGCATGAGCCAATGATTCCCTTAGGGCTCTGAGG 1861 -----+ 1920 GAGAGGGAGGAGGGGGGTGTAGGATCGTACTCGGTTACTAAGGGAATCCCGAGACTCC AAGGCAACAATGGTACCCAAGAACTGNTACGTCAGCCAGCAGGAGCTGAAGCCATTTC 1921 ------ 1980 TTCCGTTGTGTTACCATGGGTTCTTGACNATGCAGTCGGTCGTCCTCGACTTCGGTAAAG CCTTTGGTGTCCGCATTGACTACGTGCTTTACAAGGTCAGGCTCCTCCCTTCAACATGCT ---+ 2040 TTCATATGCTGTGTCTCTTTGTCTACTAACCTGTGTAGATCCTTTGCTCAGNTAGTCTAG AAGTATACGACACAGAGAAACAGATGATTGGACACATCTAGGAAACGAGTCNATCAGATC TCTTGGACCACTGATGGGTGGAAAGTGGGGTAGCCGGGAGCTGGTTCTCTGGGAAGAGGC 2101 ----- 2160 AGAACCTGGTGACTACCCACCTTTCACCCCATCGGCCCTCGACCAAGAGACCCTTCTCCG CCTCATATATAAGCTTCTCTNTGGCCCTTACTTTTCGTAGGCAGTTTCTGGGTTTTACAT GGAGTATATATTCGAAGAGANACCGGGAATGAAAAGGATCCGTCAAAGACCCAAAATGTA CTCCTGTAAGAGTTTTGAAACCACTACAGGCTTTGACCCTNACAGGGGCACCCCCCTCTC 2221 -----+ 2280 GAGGACATTCTCAAAACTTTGGTGATGTCCGAAACTGGGANTGTCCCCGTGGGGGGAGAG FIY TTGATCATGAAGCCCTGATGGCTACTCTGTTTGTGAGGCACAGCCCCCCACAGCAGAACC 2281 ----- 2340 AACTAGTACTTCGGGACTACCGATGAGACAAACACTCCGTGTCGGGGGGTGTCGTCTTGG CCAGCTCTACCCACGTGAGTCACCCCCACCCTTTCCTTGGCCCTTGCCCCGCTTGAAGC 2341 -----+ 2400 GCTCGAGATGGGTCCCACTCAGTGGGGGTGGGAAAGGAACCGGGAACGGGGCGAACTTCG AGCCCTTCCACTCTTGACTCTCCCCCCCCCCCCCCTCTCTTGTTGTAGGACCAGCAG TCGGGAAGGTGAGAACTGAGAGAGGACGGGGTGACGGGACGAGACAACATCCTGGTCGTC AGAGGTCGCCGTTGATGTGTGTGCTAAAGGAGGCCTGGACGGAGCTGGGTCTGGGCATGG 2461 -----+----+ 2520 TCTCCAGCGCAACTACACACACGATTTCCTCCGGACCTGCCTCGACCCAGACCCGTACC CTCAGGCTCGCTGGGCCCACCTTCGCTAGCTATGTGATTGGCCTGGGGCTGCTTCTCC 2521 -----+ 2580 GAGTCCGAGCGACCACCCGGTGGAAGCGATCGATACACTAACCGGACCCCGACGAAGAGG 2581 ACCGTGACGACACAGGACCGCCGACCTCCTCCCCGGCCCCTTCGACGGTATGACGAGA GGACCCCCAGTGTAGGGCTGGTGCTGTGGGCAGGTGCATTCTACCTCTTCCACGTACAGG CCTGGGGGTCACATCCCGACCACGACACCCGTCCACGTAAGATGGAGAAGGTGCATGTCC AGGTCAATGGCTTATATAGGGCCCAGGCTGAGCTCCAGCATGTGCTAGGAAGGGCAAGGG TCCAGTTACCGAATATATCCCGGGTCCGACTCGAGGTCGTACACGATCCTTCCCGTTCCC AGGCCCAGGATCTGGGCCCAGAGCCTCAGCCAGCCCTACTCCTGGGGCAGCAGGAGGGGG 2761 ------ 2820 TCCGGGTCCTAGACCCGGGTCTCGGAGTCGGTCGGGATGAGGACCCCGTCGTCCTCCCCC

ACAGAACTAAAGAACAATAAAGCT1GGCCCAA

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Figure 1-3

# Mouse Neutral Sphingomyelinase (nSMase) gene sequence

		TNGANNCTGTTAGCTCCAGNCCGGTNGGTCGCCGTNCTAGNCNNATCTNTATAGCTCTTC	
	1		
		ANCTINIGACAATCGAGGTCNGGCCANCCAGCGGCANGATCNGNNTAGANATATCGAGAAG	
		GTTGCGAGCNCAATTNNNTCTCAATAAANGGATNCANCCCTATGACAGAACGTGGACCCC	
	61	CAACGCTCGNGTTAANNNAGAGTTATTTNCCTANGTNGGGATACTGTCTTGCACCTGGGG	120
		CGCCCGCCANCNCANGNGANACCGCGGCATGGGNCTGAGGTGCNCANGGTGTCTGGGGCG	
	121		180
		GCGGGCGTNGNGTNCNCTNTGGCGCCGTACCCNGACTCCACGNGTNCCACAGACCCCGC	
		$\tt AGGGGTTACCTCAGCGATGGTCTTTGACACCTGAAAGCTGGAGCTTTTGAANAGCCCCAN$	
	181		240
		TCCCCAATGGAGTCGCTACCAGAAACTGTGGACTTTCGACCTCGAAAACTTNTCGGGGTN	
		CACCTTCAGCTTCAGGGGGGGCTCNGGCGGCAACCGCACGTGANATGCTGGGGGCTTCGA	
	241		300
		${\tt GTGGAAGTCGAAGTCCCCGCGAGNCCGCCGTTGGCGTGCACTNTACGACCCCCGAAGCT}$	
		$\tt CTTGGGCCGGCACGGNTGCTGGGTGGCCATGGAANNNACAGNACAG$	200
	301	GAACCCGGCCGTGCCNACGACCCACCGGTACCTTNNNTGTCNTGTC	360
		ATANTGCGAGTCGCCANGGNAACCGCGTGGCTCCTCCCCGAACGCCCNCAAGGGGCGGGA	
	361		420
		TATNACGCTCAGCGGTNCCNTTGGCGCACCGAGGAGGGGCTTGCGGGGNGTTCCCCGCCCT	
		${\tt CCTGAGTGAGTTCNTGGGGGGGGCCTCNCATCAACTTCAAGCCTGTTGCTGGTGGAAGCC}$	
	421		480
		GGACTCACTCAAGNACCCGCCCCGGAGNGTAGTTGAAGTTCGGACAACGACCACCTTCGG	
÷.		${\tt GAGCCGGGAACAAGGGAGGAACCTGTAGGCCGCGGTGCGGATAACCCACCGAAGGACCTA}$	
ΕI	481		540
		CTCGGCCCTTGTTCCCTCCTTGGACATCCGGCGCCACGCCTATTGGGTGGCTTCCTGGAT	
		${\tt AGAATCTGGAACAGTCCACCCGAGATTCCTTCCAGGACTGCCGGCGGACTCTCGCATTCA}$	
	541	+	600
		TCTTAGACCTTGTCAGGTGGGCTCTAAGGAAGGTCCTGACGGCCGCCTGAGAGCGTAAGT	
		${\tt GCCCGGGATTTGCAGCCGACCTTCTTTCCGGGTGGAATGACGGCCTTTGTCCCAGTAACG}$	cc.
	601		660
		CGGGCCCTAAACGTCGGCTGGAAGAAAGGCCCACCTTACTGCCGGAAACAGGGTCATTGC	
		CAGGAGTCHNCCCCCACCCCCAACCAGCTCGCGTTCCTGGGTCGGGGCAGCGCAGGATAGG	
	661		720
		GTCCTCAGNNGGGGTGGGGGTTGGTCGAGCGCAAGGACCCAGCCCCGTCGCGTCCTATCC Start	:
	777	GCAATAAGCCTGTGCGCGCAATCCGCCTCGCCGCCCTTGCTCCGAAGCACTCCAGCCATG	780
	,21	CGTTATTCGGACACGCGCGTTAGGCGGAGCGGCGGGAACGAGGCTTCGTGAGGTCGGTAC	
		AAGCTCAACTTTTCTCTACGGCTGAGAGTTTTCAATCTCAACTGCTGGtaagtaagtgct	
	781		840

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841		cccaggegtgggCTGCAGCCTCGGAGCCACCTTCCAGTCCCCTCTCGCACATGCCTAGGA	
		${\tt gggtccgcacccGACGTCGGAGCCTCGGTGGAAGGTCAGGGGAGAGCGTGTACGGATCCT}$	
901		AGGAAGCAGGTCTTCTCAGCCGAGCTAGACCCTGTCCTTCCCGAACCACCAAAGTCCAC	960
	,,,	${\tt TCCTTCGTCCAGAAGAAGTCGGCTCGATCTGGGACAGGAAGGGCTTGGTGGTTTCAGGTG}$	
	961	ATCGCCTAAAGACCAGAGCTTGGGTGGTTGCAGCAATCACCAAAGTCCCTATCATCCAAA	1020
	701	TAGCGGATTTCTGGTCTCGAACCCACCAACGTCGTTAGTGGTTTCAGGGATAGTAGGTTT	2020
		GCTGAGGTGATGACAGCAGTAATCGTCCCAAACCTGGCCCATGTCTTTCCTTTTAAATGA	1000
	1021	CGACTCCACTACTGTCGTCATTAGCAGGGTTTGGACCGGGTACAGAAAGGAAAATTTACT	1000
	2002	TTTACTTTTATTTTATGTACATTTGGTGTTTTTGCCTGTATGTA	1140
	1081	AAATGAAAATAAAATACATGTAAACCACAAAACGGACATACAT	11,0
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	1141	GTCTAAGAGACCCTGACCTCAATGTCTGTCAACATTCGACAGTACACGAACGA	1200
		GAACTGCTGACCCATCTCTTCTGCCCCCTGCGTCCTCCACCCCTTTTAGGGACATCCCCT	
	1201	CTTGACGACTGGGTAGAGAAGACGGGGGGAACGCCAGGAGGTGGGGAAAATCCCTGTAGGGGA	1260
		ACCTGAGCAAACATAGGGCGGACCGCATGAAGCGCTTGGGAGACTTTCTGAACTTGGAAA	
		TGGACTCGTTTGTATCCCGCCTGGCGTACTTCGCGAACCCTCTGAAAGACTTGAACCTTT	1320
Ц			
**		ACTITGATCTGGCTCTCCTGGAGGAGGTGAGGTTGTAGGCCAGGCTAGGTTGGAGGAGGG	
**		ACTTTGATCTGGCTCTCCTGGAGGAGGTGAGGTTGTAGGCAGGC	1380
**	1321	TGARACTAGACCGAGAGGGCCTCCTCCACTCCAACATCCGGTCCGATCCAACCTCCTCCCCCAGCAGGCAG	
*1	1321	TGAAACTAGACCGAGAGGACCTCCTCCACTCCAACATCCCGTCCGATCCAACCTCCTCCC	
**	1321	TGAAACTAGACCGAGGGGACCTCCTCCACTCCAACATCCGTCCG	1440
	1321 1381 1441	TGAAACTAGACCGAGGGGACCTCCTCCACTCCAACATCCGTCCG	1440
u	1321 1381 1441	TGRANCTAGACCGAGAGGACCTCCTCACTCCACCTCCACCTCCGATCCAACCTCCACCTCCCCCCAGCAGGACACCTCCTCCACCTCCACCTCCACCTCCAACCTCCAACCTCCAACCTCCAACCTCCAACCTCCAACCTCCAACCTCCACCTTCTAGACAAGACAGAACCCTACTTTAGGGTTCGTTC	1440
	1321 1381 1441 I	TGRANCTAGNOCGAGAGGACCTCCTCCACTCCACCTCCGTCCGTTCCAACCTCCTCCCC CAGCAGGCGGCAGGACAACTTGTTCTGTCTTGGGATGAAATCCCAAGCCA CTCGTCCGCCGTCCGCGCGTCCTTTTGAACAAGACAGAACCCTACTTTAGGGTTCGTT GTATCCTCACCTTCTTCCTCCAGGTGTGGAGTGAGCAGGACTTCCCAGTACCTAAGGCAA CATAGGAGTGGAAGAAGGAGGACTTCCTCACTCTCTCTTAGGATACCTTA	1440 1500
	1321 1381 1441 I	TGARACTAGACCGAGAGGACCTCCTCCACTCCAACATCCGTCCG	1440 1500
	1321 1381 1441 I	TGAAACTAGACCGAGGGGCCTCCTCCACTCCAACATCCGTCCG	1440 1500
	1321 1381 1441 I 1501	TGARACTAGACCGAGAGGACCTCCTCCACTCCAACATCCGTCCG	1440 1500
	1321 1381 1441 I 1501	TGAAACTAGACCGAGAGGACCTCCTCAACATCCGTCCGATCCAACCTCCCTC	1440 1500 1560
	1321 1381 1441 I 1501	TGANACTAGACCGAGAGGACCTCCTCCACCTCCAACATCCGGCCAACCTCCAACCTCCTCCCCCCGCGCGCAGGAAAACTTGTTCTGCTCTGGGATAAAATCCCAAGCAACCTCCTCGTGCGCGCGC	1440 1500 1560
	1321 1361 1441 I 1501	TGAAACTAGAACGAGAGGACCTCCTCCACCTCCAACATCCGGCCAACCTCCAACCTCCTCCCCCCAACACACCTCGACAACCCTCCTCCCCCCAACACACAC	1440 1500 1560

	1741	GGGTACTCCCCTCCTTGCTCTCTGGTTATTAAGCAAGAGTTGGTTTTCAGCGGGATGAT	1800
Εľ	V	CCCATGAGGGGAGGAACGAGAAGACCAATAATTCGTTCTCAACCAAAAGTCGCCCTACTA	
	1801	AGGCAGTGGCCTCTGTGTGTTCTCCAAACACCCAATCCAGGAAATCTTCCAGCATGTCTA	1860
	1861	CAGTCTGAATGGTTACCCCTACATGGTAAGGATCTCTTCCCTATCCTTGCTAACACAGAC GTCAGACTTACCAATGGGATGTACCATTCCTAGAGAAGGAATAGGAACGATTGTGTCTC	
	1921	TGGACGCAGCCTTCCTGGGGGCCTTGGCAGGAGGGGTGTCAGTACCCTGAGTTTTTGTCTTC	
		TCTTGCCTGCAGTTCCATCATGAGAGACTGGTTCTGTGGGAAAGTCTGTGGGGCTGCTGGTG	2040
Eν		CTCCGTCTAAGTGGACTGGTGCTCAATGCCTACGTGACTCATGTGAGTGGGGCTAGCCAG GAGGCAGATTCACCTGACCACGAGTTACGGATGCACTGAGTACACTCACCCCGATCGGTC	2100
	2101	GCTTAGGCAGTGGGTCAAGCAGCCCAATGCTATGGTGGAGAAGAGACGCCACTAGTTAGT	2160
	2161	TCTGCTGCCTGGGGATAAGGCATGGGATCAGAAGCTAGCATTGGGCAAGGTTCACCCATT AGACGACGGACCCCTATTCCGTACCCTAGTCTTCGATCGTAACCCGTTCCAAGTGGGTAA	2220
	2221	CCCTGTCACACTCTGCCATGTGACAGATGACAAGCTTGATTCAGACAGCCTTCTCTTTGA	2280
ΕV		TTTCACCTATTCCACTTTAGCTACATGCTGAGTACAGCCGACAGAAGGACATCTACTTTG	2340
E V	-	CACACCGTGTGGCCCAAGCTTGGGAACTGGCCCAGTTCATCCAGTGTGAGCCTGGGCT GTGTGGCACACCGGGTTCGAACCCTTGACCGGGTCAAAGTAGGTCACACACTCGGACCCGA	2400
	2401	TGATGGGGCTGTGGGGTGGGGACGGGTTGAGGGATGNGNANTTATCCTTGAAGAGGG	2460
		CACATAATAAGGGAAGAATTTCCTCCTTGCCGCTCTTCCCCCAACTCAGCCACACATCCA GTGTATTATTCCCTTCTTAAAGGAGGAACGGCGAGAAGGGGGTTGAGTCGGTGTGTAGGT	
EV		AGAATGCAGATGTGGTTCTATTGTGGGAGACCTCAATATGCACCCCAAAGACCTGGGCT  ******************************	2580
		T' O O	

	25.03	GCTGCCTGCAAAGAGTGGACAGGGCTCCATGATGCTTTCGTTGAGACTGAGGACTTTA	
	2501	CGACGGACGACTTTCTCACCTGTCCCGAGGTACTACGAAAGCAACTCTGACTCCTGAAAT	2040
	2641	AGGTGAGAGACTGTTTCCCACCAACTCCACCACTTGTTCCAGTCTTCCTGTCTCTTAGCAT	2700
		${\tt TCCACTCTGACAAAGGGTGGTTGAGGTGTGAACAAGGTCAGAAGGACAGAGAATCGTA}$	
	2701	CCTAGCCACCTGTTTCCCTAGGGCTCTGATGATGGTGCCTATGGTACCCAAGAACTGC	2760
ΕV		${\tt GGATCGGTGGACAAAGGGATCCCGAGACTACTACCGACATGGTACCATGGGTTCTTGACG}$	
15 1	,,,	TACGTCAGCCAGCAGGACCTGGGACCGTTTCCGTCTGGTATCCGGATTGATT	
	2761	ATGCAGTCGGTCGTGGACCCTGGCAAAGGCAGACCATAGGCCTAACTAA	2820
		TACAAGGTCAGGCTCTTATTCCCGGTGTGCCTTCTCCAGTATCTTCCTTC	
	2821		2880
		ATGTTCCAGTCCGAGAATAAGGGCCACACGGAAGAGGTCATAGAAGGAAG	
		$\tt AGCCCACGCTTTAGTTCAGCTACAGTCTTGGGCCACTGATGGCTAAAGAATAGAATCCTG$	
	2861	TCGGGTGCGAAATCAAGTCGATGTCAGAACCCGGTGACTACCGATTTCTTATCTTAGGAC	2940
		TCGGCTGGTTCTCTGGGAGAATTTAAGCTTCTCCATGTTCTTGCTCTTCCTAGGCAGTCT	
	2941	AGCCGACCARGAGACCCTCTTAAATTCGAAGAGGGTACAAGAACGAGAAGGATCCGTCAGA	3000
		CTGAGTTCCACGTCTGCTGAGACTCTGAAAACCACTACAGGCTGTGACCCTCACAGTG	
	3001		3060
ΕD		GACTCAAGGTGCAGACGACACTCTGAGACTTTTGGTGATGTCCGACACTGGGAGTGTCAC	
		ACAAGCCCTTCTCTGATCACGAGGCCCTCATGGCTACTTTGTATGTGAAGCACAGCCCCC	
	3061	TGTTCGGGAAGAGTAGTGCTCCGGGAGTACCGATGAAACATACACTTCGTGTCGGGGG	3120
		CTCAGGAAGACCCCTGTACTGCCTGTGGTAAGCAGCATTTCCTTTGCCCCCCTCTACTTTA	
	3121	GAGTCCTTCTGGGGACATGACGGACACCCATTCGTCGTAAAGGAAACGGGGGAGATGAAAT	3180
		AGGCAGCCCGCCTCCATCCTGACCCTCCCCTGCTCTACGTTCTCTCTTTTTCCAGGCCC	
	3181		3240
		TCCGTCGGGCGGAGGTAGGACTGGGAGGGACGAGATGCAAGAGAGAAAAAAGGTCCGGG	
		ACTGGAAAGGTCCGATTTGATCAGCGTGCTAAGGGAGGCCAGGACAGAGCTGGGGCTAGG	3300
	3241	TGACCTTTCCAGGCTAAACTAGTCGCACGATTCCCTCCGGTCCTGTCTCGACCCCGATCC	3300
EΧ		CATAGCTAAAGCTCGCTGGTGGGCTGCATTCTCTGGCTATGTGATCGTTTTGGGGGCTGTC	
	3301		3360
		GTATCGATTTCGAGCGACCACCCGACGTAAGAGACCGATACACTAGCAAACCCCCGACAG	
	3361	CCTTCTGGTGTTGCTGTGTCCTGGCTGCAGGAGAAGAGGCCAGGGAAGTGGCCATCAT	3420

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	CCTCTGCATACCCAGTGTGGGTCTGGTGCTGGTAGCAGGTGCAGTCTACCTCTTCCACA		
3423			
	GGAGACGTATGGGTCACACCCAGACCACGACCATCGTCCACGTCAGATGGAGAAGGTGTT		
3401	GCAGGAGGCCAAGGGCTTATGTCGGGCCCAGGCTGAGATGCTGCACGTTCTGACAAGGGA		
3401	CGTCCTCCGGTTCCCGAATACAGCCCGGGTCCGACTCTACGACGTGCAAGACTGTTCCCT		
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3541		3600	
	TTGCCTCTGGGTCCTGGCTCCGAGTCTCGGAGTGGATCGGATGACGAACGTCGTCCTCCC	GGTCCTGGCTCCGAGTCTCGGAGTGGATCGGATGACGAACGTCGTCCTCCC stop	
2000	GGACAGAGC <u>TTA</u> AGAGCTTAACAATAAAACTTGCTTGACACACTCTAGTGGCTCTACCTT		
3601	CCTGTCTCGAATTCTCGAATTGTTATTTTGAACGAACTGTGTGAGATCACCGAGATGGAA		
3661	GTTCCTTGCAGAGGCATGATGGGAACTGAAGGTCAGTGGCCTTGTCACTGTGTGGCTTTA		
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3721	+		
	CTCGCAACCGGAGAGTGAACGGAAAAAACGTGTGAGGGCAGAGGACGGTCGTGTCTCGTA		
	${\tt AAACCCTGTTCATGGTCATAATCCTTTTATTGTAAACAACGAAGCCTCTGACTAAGCAGT}$		
3781			
	TTTGGGACAAGTACCAGTATTAGGAAAATAACATTTGTTGCTTCGGAGACTGATTCGTCA		
	$\tt CCAGATGGCGGAGGTACAGCCCTTGTGATGGTGTCTTGCTTACGGGGCAGGGAGGCAGCT$		
3841		3900	
	GGTCTACCGCCTCCATGTCGGGAACACTACCACAGAACGAATGCCCCGTCCCTCCGTCGA		
	${\tt AACCATCATCTTCTAGCCCTGGGCTCCCATCTATGCAGGCATCTCTCTGAGCCTCCGTTC}$		
3901	TTGGTAGTAGAAGATCGGGACCCGAGGGTAGATACGTCCGTAGAGAGACTCCGGAGGCAAG	3960	
	TIGGTAGTAGAAGATCGGGACCCGAGGGTAGATACGTCCGTAGAGAGACTCGGAGGCAAG		
	CTCCTGGAATTGGNTCAGAGCAATCCCGCTTGGTTCACCAACCTCCAAACAGCTTCCTTA		
3961	CACCACCOURA A CONTA CONTRA COCCOCA A COCA A	4020	
	GAGGACCTTAACCNAGTCTCGTTAGGGCGAACCAAGTGGTTGGAGGTTTGTCGAAGGAAT		
	${\tt AGGACCTGGTTTCTCAAAANGGNAAGGTNCGGGCCTCCGGTCTTCAATANGTTTTCCTAA}$		
4021	TCCTGGACCAAAGAGTTTTNCCNTTCCANGCCCGGAGGCCAGAAGTTATNCAAAAGGATT	4080	
	AAAGGGANGAATGAAAANCCTTAAGNNCCAACAAGGGGAACCCTTGGNCCCAAAAGGGGA		
4081	######################################	4140	
	TTTCCCTNCTTACTTTTNGGAATTCNNGGTTGTTCCCCTTGGGAACCNGGGTTTTCCCCT		
4744	CCTGGGTGGTTTCCCNTTGGGGCCAAANTTATCCCAAAGGGGTCCAATTGAAGGGTTAAC	4200	
4141	GGACCCACCAAAGGGNAACCCCGGTTTNAATAGGGTTTCCCCAGGTTAACTTCCCAATTG	4200	
4202	CCCCCAAAAANNACCGNTTTCCCCCGGGAATTTCCAAAGGTTTNCCCCCCCCGGGCAAAANC	4360	
4201	GGGGGTTTTTNNTGGGNAAAGGGGGCCTTAAAGGTTTCCAAANGGGGGGGCCCGTTTTNG	4200	

4261	TCCCTTGGGGNNCCNAANCCNTGGCCCGGNCTTGGCTTTTCCCCCTTTCCCAAGNATTTC  AGGGAACCCCNNGGNTINGGNACCGGGCCNGAACCGAAAAGGGGGAAAAGGGTTCNTAAAG	4320
4321	AAANNTTCCCTNGGAAANCCCCTTGNTTGGNAAAACCNAATNANGAACCAAGCCAANNNT TTTINNAAGGANCCTTTNGGGGAACNAACCNTTTTGGNTTANTNCTTGGTTCGGTTNNNA	4380
4381	$\begin{tabular}{ll} TGCCAANAAACCNTTTGGGCAAAGGGGGAAATTCANCAANGGGGNAATTGGGGAAACCC \\$	4440
4441	NTGGGTTTNCCCAAAGGGCCCNAANANT	

Figure 2-6

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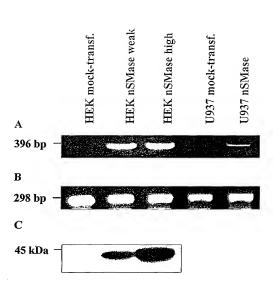


Figure 3

mnSMase "konventional" Knock Out

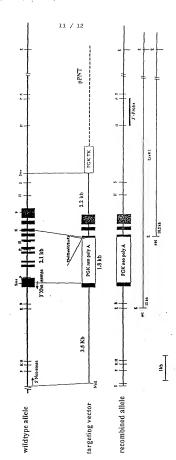


Figure 4

## Constructs for generating transgenic mouse mutants

1	ubiquitin promoter	nSMase	IRES	lacZ	polyA	

polyA	rtTA	CMV	CMV-1	nSMase	IRES	GFP	polyA

Ubiquitin promoter: regulatory sequence of the ubiquitin gene, controlling

a ubiquitous transcription.

nSMase: neutral sphingomyelinase

lacZ:

lacZ, gene coding for β-galactosidase

recognition signal for the termination of transcription polyA: and polyadenylation

CMV: cytomegalovirus promoter of the cytomegalovirus

gene, controlling a ubiquitous transcription.

reverse transactivator, binds to the minimal promoter rtTA:

and thus controls transcription. The binding properties of the transactivator are influenced by tetracyclin. The addition of tetracyclin makes the transactivator bind to the minimal promoter and starts transcription, removal of tetracyclin prevents the binding of the transactivator to the minimal promoter and prevents tran-

scription.

CMV-1: minimal promoter, binding of transactivator starts

transcription.

IRES: internal ribosomal entry sequence, viral initiation

signal for translation.